

10	30	50
CATGGGTGGGGGTGGGGGCGCTGCTGGATTCTGCTCTGGTGGAGGGGAACTTGTGAGG		
70	90	110
GGCTGGTAAGCGCCCCCTCCGAAGCCTGGTGTGTGCGCGGGGGGAAGGAAGTTAGTTTCC		
130	150	170
TCTCCACCCATGGGCACCCCTTCTGCCCCGGGGCCTGGGAAGTGGGCTGCTCTGTGGGCAA		
190	210	230
ATGCTGGGGCCTCTGAAATGGAGGAGACGCAGCAGGGAGAGGCCCCACGTGGGCAGCTGC		
<u>M E E T Q Q G E A P R G Q L R</u>		
250	270	290
GCGGAGAGTCAGCAGCACCTGTCCCCAGGCGCTCCTCCTGGTGTGCTGCTGGGGGCCCCGGG		
<u>G E S A A P V P Q A L L L V L L G A R A</u>		
310	330	350
CCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTG		
Q G G T R S P R C D C A G D F H K K I G		
370	390	410
GTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCTTGCACGGAGC		
L F C C R G C P A G H Y L K A P C T E P		
430	450	470
CCTGCGGCAACTCCACCTGCCTTGTGTGTCCCCAAGACACCTTCTTGGCCTGGGAGAACC		
C G N S T C L V C P Q D T F L A W E N H		
490	510	530
ACCATAATTCTGAATGTGCCCCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGC		
H N S E C A R C Q A C D E Q A S Q V A L		
550	570	590
TGGAGAACTGTTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGG		
E N C S A V A D T R C G C K P G W F V E		
610	630	650
AGTGCCAGGTCAGCCAATGTGTGCAGCAGTTCACCCTTCTACTGCCAACCATGCCTAGACT		
C Q V S Q C V S S S P F Y C Q P C L D C		

FIG.1A

670	690	710
GCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACTGACTGTGGGA		
G A L H R H T R L L C S R R D T D C G T		
730	750	770
CCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGCACCC		
C L P G F Y E H G D G C V S C P T S T L		
790	810	830
TGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAGATGTTCTGGGTCC		
G S C P E R C A A V C G W R Q M F <u>W V Q</u>		
850	870	890
AGGTGCTCCTGGCTGGCCTTGTGGTCCCCCTCCTGCTTGGGGCCACCCTGACCTACACAT		
<u>V L L A G L V V P L L L G A T L T Y T Y</u>		
910	930	950
ACCGCCACTGCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTC		
R H C W P H K P L V T A D E A G M E A L		
970	990	1010
TGACCCACACACCGGCCACCCATCTGTACCCCTTGGACAGCGCCACACCCTTCTAGCAC		
T P P P A T H L S P L D S A H T L L A P		
1030	1050	1070
CTCCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTG		
P D S S E K I C T V Q L V G N S W T P G		
1090	1110	1130
GCTACCCCGAGACCCAGGAGGCGCTCTGCCCAGGTGACATGGTCCTGGGACCAGTTGC		
Y P E T Q E A L C P Q V T W S W D Q L P		
1150	1170	1190
CCAGCAGAGCTCTTGGCCCCGCTGCTGCGCCACACTCTCGCCAGAGTCCCCAGCCGGCT		
S R A L G P A A A P T L S P E S P A G S		
1210	1230	1250
CGCCAGCCATGATGCTGCAGCCGGGCGCAGCTCTACGACGTGATGGACGCGGTCCCAG		
P A M M L Q P G P Q L Y D V M D A <u>V P A</u>		
1270	1290	1310
CGCGGCGCTGGAAGGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCG		
<u>R R W K E F V R T L G L R E A E I E A V</u>		

FIG.1B

1330	1350	1370
TGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCC		
<u>E V E I G R F R D Q Q Y E M L K R W R Q</u>		
1390	1410	1430
AGCAGCAGCCCGCGGGCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACG		
<u>Q Q P A G L G A V Y A A L E R M G L D G</u>		
1450	1470	1490
GCTGCGTGGAAGACTTGCGCAGCCGCTGCAGCGCGGCCCGTGACACGGCGCCCACTTGC		
<u>C V E D L R S R L Q R G P *</u>		
1510	1530	1550
CACCTAGGCGCTCTGGTGGCCCTTGCGAAGCCCTAAGTACGGTTACTTATGCGTGTAGA		
1570	1590	1610
CATTTTATGTCACTTATTAAGCCGCTGGCACGGCCCTGCGTAGCAGCACCAGCCGGCCCC		
1630	1650	1670
ACCCCTGCTCGCCCCTATCGCTCCAGCCAAGGCGAAGAAGCACGAACGAATGTCGAGAGG		
1690	1710	1730
GGGTGAAGACATTTCTCAACTTCTCGGCCGGAGTTTGGCTGAGATCGCGGTATTAAATCT		
1750	1770	
GTGAAAGAAAACAAAACAAAACAAAAAAAAAAAAAAAAAAAAA		

FIG.1C

1 ATGGAGCAGC GGCCGCGGGG CTGCGCGGCG GTGGCGGCGG CGCTCCTCCT GGTGCTGCTG
 M E Q R P R G C A A V A A A L L L V L L

61 GGGGCCCCGG CCCAGGCGG CACTCGTAGC CCCAGGTGTG ACTGTGCCGG TGAATTCCAC
 G A R A Q G G T R S P R C D C A G D F H

121 AAGAAGATTG GTCTGTTTTG TTGCAGAGGC TGCCCAGCGG GGCACCTACCT GAAGGCCCTT
 K K I G L F C C R G C P A G H Y L K A P

181 TGCACGGAGC CCTGCGGCAA CTCCACCTGC CTTGTGTGTC CCCAAGACAC CTTCTTGGCC
 C T E P C G N S T C L V C P Q D T F L A

241 TGGGAGAACC ACCATAATTC TGAATGTGCC CGCTGCCAGG CCTGTGATGA GCAGGCCTCC
 W E N H H N S E C A R C Q A C D E Q A S

301 CAGGTGGCGC TGGAGAACTG TTCAGCAGTG GCCGACACCC GCTGTGGCTG TAAGCCAGGC
 Q V A L E N C S A V A D T R C G C K P G

361 TGGTTTGTGG AGTGCCAGGT CAGCCAATGT GTCAGCAGTT CACCCTTCTA CTGCCAACCA
 W F V E C Q V S Q C V S S S P F Y C Q P

421 TGCCTAGACT GCGGGGCCCT GCACCGCCAC ACACGGCTAC TCTGTTCCCG CAGAGATACT
 C L D C G A L H R H T R L L C S R R D T

481 GACTGTGGGA CCTGCCTGCC TGGCTTCTAT GAACATGGCG ATGGCTGCGT GTCCTGCCCC
 D C G T C L P G F Y E H G D G C V S C P

541 ACGAGCACCC TGGGGAGCTG TCCAGAGCGC TGTGCCGCTG TCTGTGGCTG GAGGCAGATG
 T S T L G S C P E R C A A V C G W R Q M

601 TTCTGGGTCC AGGTGCTCCT GGCTGGCCTT GTGGTCCCC TCCTGCTTGG GGCCACCCTG
 F W V Q V L L A G L V V P L L L G A T L

661 ACCTACACAT ACCGCCACTG CTGGCCTCAC AAGCCCCTGG TTAAGCTGGA TGAAGCTGGG
 T Y T Y R H C W P H K P L V T A D E A G

721 ATGGAGGCTC TGACCCACCC ACCGGCCACC CATCTGTCAC CCTTGGACAG CGCCACACCC
 M E A L T P P P A T H L S P L D S A H T

781 CTTCTAGCAC CTCCTGACAG CAGTGAGAAG ATCTGCACCG TCCAGTTGGT GGGTAACAGC
 L L A P P D S S E K I C T V Q L V G N S

FIG.2A

841 TGGACCCCTG GCTACCCCGA GACCCAGGAG GCGCTCTGCC CGCAGGTGAC ATGGTCCTGG
 W T P G Y P E T Q E A L C P Q V T W S W
 901 GACCAGTTGC CCAGCAGAGC TCTTGGCCCC GCTGCTGCGC CCACACTCTC GCCAGAGTCC
 D Q L P S R A L G P A A A P T L S P E S
 961 CCAGCCGGCT CGCCAGCCAT GATGCTGCAG CCGGGCCCCG AGCTCTACGA CGTGATGGAC
 P A G S P A M M L Q P G P Q L Y D V M D
 1021 GCGGTCCCAG CGCGGCGCTG GAAGGAGTTC GTGCCGACGC TGGGGCTGCG CGAGGCAGAG
 A V P A R R W K E F V R T L G L R E A E
 1081 ATCGAAGCCG TGGAGGTGGA GATCGGCCGC TTCCGAGACC AGCAGTACGA GATGCTCAAG
 I E A V E V E I G R F R D Q Q Y E M L K
 1141 CGCTGGCGCC AGCAGCAGCC CGCGGGCCTC GGAGCCGTTT ACGCGGCCCT GGAGCGCATG
 R W R Q Q Q P A G L G A V Y A A L E R M
 1201 GGGCTGGACG GCTGCGTGGA AGACTTGCGC AGCCGCCTGC AGCGCGGCCG GTGA
 G L D G C V E D L R S R L Q R G P

FIG.2B

[illegible]

FIG. 3A

Consensus #1 T . C . C	
DDCR	S A V A D T R C G C K P G W F V E C - - - Q V S Q C V S S S	145
TNFR1	T V D R D T V C G C R K N Q Y R H Y W S E N L F Q C - - -	144
FAS	I R T Q N I I K C R C K P N F F Q N - - - - -	137
Consensus #1 C	
DDCR	P F Y C Q Q P C L D C G A L H R H T R L L C S R R D T D C G T	175
TNFR1	- F N C S L C L N - G T V H - - - L S C Q E K Q N T V C T	167
FAS	- - - S T V C E H C D P - - - - - C T K	148
Consensus #1	C C	
DDCR	C L P G F Y E H G D G C V S C P T S T L G - S C P E R C - -	203
TNFR1	C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P	197
FAS	C E H G I I - - - K E C - - - - - T L T S N T K C - -	166
Consensus #1 L	
DDCR	- - - - - A A V C G W R Q M F W V Q V L L A G L V V P L	225
TNFR1	Q I E N V K G T E D S G T T V L L P L V I F F G L C L L S L	227
FAS	- - - - - K E E G S R S N L G W L C L L - - L P I P L	186

FIG.3B

Consensus #1K.FV	
DDCR	--PAMMLQPGPQLYDVMDAVPPARRWKEFV	362
TNFR1	HKPSLTDDPATLYAVVENVPPLRWKEFV	375
FAS	-----DVDSLKYITTIAGVMTLSQVKGFV	249
Consensus #1	R.G.....L.	
DDCR	RTLGLREAEIEAVEVEIGR-FRQQQYEMLK	391
TNFR1	RRLLGLSDHEIDRLQLQNGRCCLRERAAQYSMLA	405
FAS	RKNGVNEAKIIDIEIKNDNVQDTAEQKVKLLR	279
Consensus #1	W.....A.....L.....L.....E	
DDCR	RWRQQQP--AGLGA VYAALERMGLDGCVE	418
TNFR1	TWRRTTPRREATLELLGRVLLRDMDDLGLCE	435
FAS	NWHQLHGKKEA-YDTLLIKDLLKKNLCTLAEE	308
Consensus #1	
DDCR	DL-----RSLQRCGP	428
TNFR1	DIEEAL-----CGPAALLPPAPSLR	455
FAS	KIQTIILKDIITSDSENSNFRNEIQSLV	335

FIG.3D

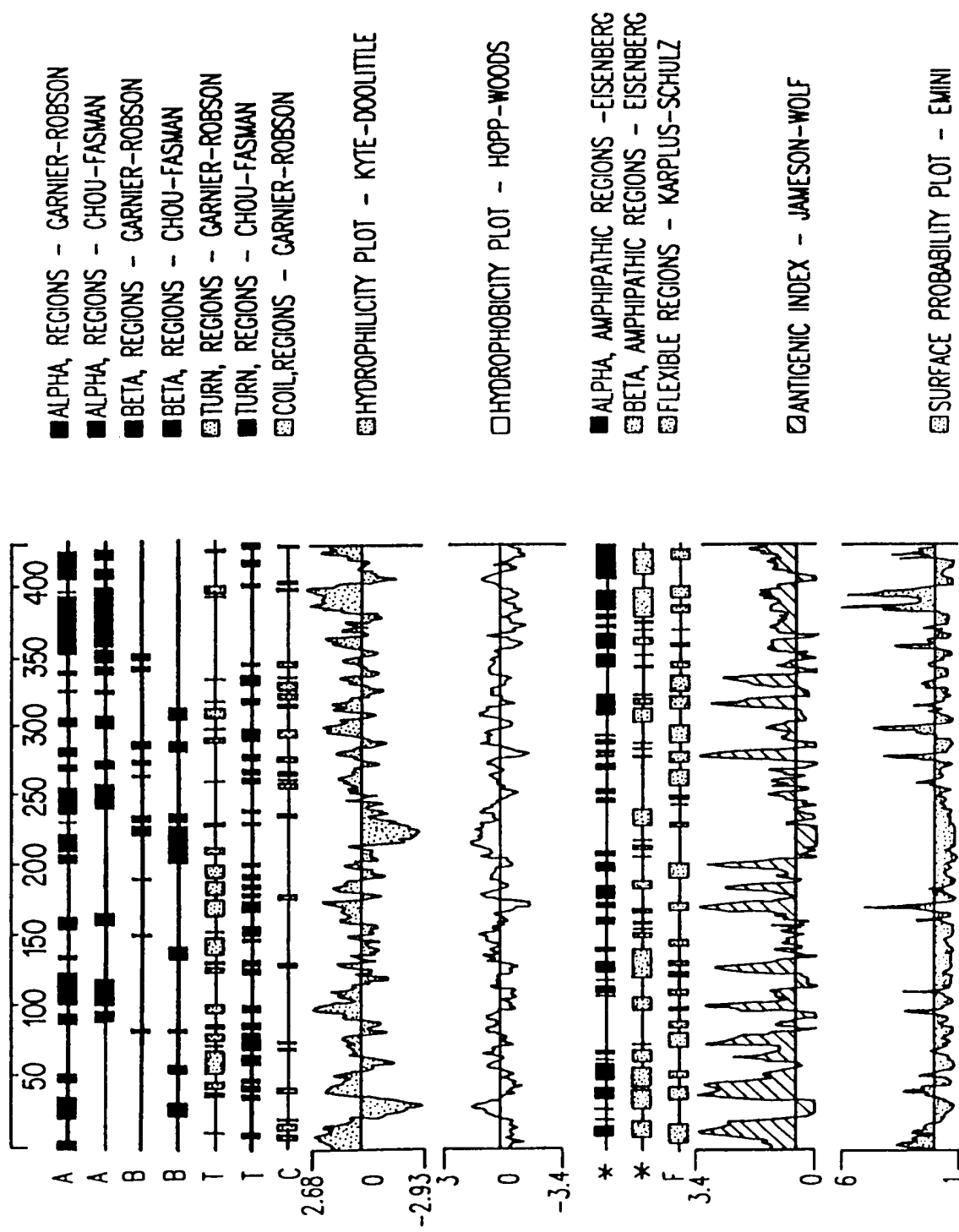


FIG. 4